



Replacement Sheet

FIGURE 6A

1. 'A' Allele, CYP2D6\*3, A21337 deletion, Frameshift resulting in zero enzyme activity

SEQ ID NO:6 5'- GCTAACTGAGCACAGGATGACC -3' NH2 CYPwt (+)A2624, 22mer, 54%GC, Tm=63-64C  
SEQ ID NO:7 5'- GCTAACTGAGCACAGGATGACC (A) 30 -3' NH2 CYPwt (+)A2624 (A) 30-3'NH2  
SEQ ID NO:8 5'- CTAACTGAGCACAGGATGACC (A) 30 -3' NH2 CYPwt (+)A2625 (A) 30-3'NH2  
SEQ ID NO:9 5'- CTAACTGAGCACAGGATGACC (A) 30 -3' NH2 CYPwt (+)A2625b (A) 30-3'NH2  
SEQ ID NO:10 5'- GCTAACTGAGCAC-GGATGACC -3'NH2 CYPmut (+)A2624, 21 mer, 57%GC, Tm=61-63C  
SEQ ID NO:11 5'- GCTAACTGAGCAC-GGATGACC (A) 30 -3' NH2 CYPmut (+)A2624 (A) 30-3'NH2  
SEQ ID NO:12 5'- CTAACTGAGCAC-GGATGACC (A) 30 -3' NH2 CYPmut (+)A2625 (A) 30-3'NH2  
SEQ ID NO:13 5'- CTAACTGAGCAC-GGATGACC (A) 30 -3' NH2 CYPmut (+)A2625b (A) 30-3'NH2

|-2612

SEQ ID NO:14 5'- GCTGGATGAGCTGCTAACTGAGCACAGGATGACCTGGACCCAGCCAGCC -3' Wild Type (+)  
SEQ ID NO:15 5'- GCTGGATGAGCTGCTAACTGAGCAC-GGATGACCTGGACCCAGCCAGCC -3' Mut (+)

2. 'B' Allele, CYP2D6\*4, G1934A, Spliceing defect resulting in zero enzyme activity

A. wt Probe - CYPwt (-)B1922 (C/A to mut at base 5) & CYPmut (+)B1922 (A/C to mut at base 13)

1934

SEQ ID NO:16 NH2 3'- GAGGGTGGGGTCTCTGC -5' CYPwt (-)B1922, 17mer, 76%GC, Tm=66C  
SEQ ID NO:17 5'- CTCCCACCCCCAGGACG -3'NH2 CYPwt (+)B1922-Target  
SEQ ID NO:18 5'- CTCCCACCCCCAAGACG -3' NH2 CYPmut (+)B1922, 17mer, 71%GC, Tm=58-60C  
SEQ ID NO:19 NH2 3'- GAGGGTGGGGTCTCTGC -5' CYPmut (-)B1922- Target

|-1909

SEQ ID NO:20 5'- CCCTTACCCGATCTCCACCCCCCAGGACGCCCTTTCGCCCAACGGTCT -3' WildType (+)  
SEQ ID NO:21 5'- CCCTTACCCGATCTCCACCCCCCAGGACGCCCTTTCGCCCAACGGTCT -3' Mut (+)

B. CYPwt (-)B1930 (C/A to mut at base 13) and CYPmut (+)B1930 (A/C to wt at base 5)

SEQ ID NO:22 NH2 3'- GGGTCTCGGGGAAAG -5' CYPwt (-) B1930, 17mer, 71%GC, Tm=56C  
SEQ ID NO:23 NH2 3'- (A)30GGGTCTCGGGGAAAG -5' CYPwt (-) B1930 (A) 30-3'NH2  
SEQ ID NO:24 5'- CCCAAGACGCCCTTTC -3' NH2 CYPmut (+)B1930, 17mer, 65%GC, Tm=54C  
SEQ ID NO:25 5'- CCCAAGACGCCCTTTC (A) 30 -3' NH2 CYPmut (+)B1930 (A) 30-3'NH2

|-1909

SEQ ID NO:26 5'- CCCTTACCCGATCTCCACCCCCCAGGACGCCCTTTCGCCCAACGGTCT -3' Wild Type (+)  
SEQ ID NO:27 5'- CCCTTACCCGATCTCCACCCCCCAGGACGCCCTTTCGCCCAACGGTCT -3' Mut (+)

Replacement Sheet

FIGURE 6B

3. 'C' Allele, CYP2D6\*9, G2702-A2704 deletion, decreased enzyme activity

SEQ ID NO:28 5'- GCAGAGATGGAGAAGGTGAGAG -3' NH2 CYPwt (+) C2691, 22mer, 55%GC, Tm=60C  
SEQ ID NO:29 5'- GCAGAGATGGAGAAGGTGAGAG (A) 30 -3' NH2 CYPwt (+) C2691 (A) 30-3' NH2  
SEQ ID NO:30 5'- CAGAGATGGAGAAGGTGAGAG (A) 30 -3' NH2 CYPwt (+) C2692 (A) 30-3' NH2  
SEQ ID NO:31 5'- GCAGAGATGGA---GGTGAGAGTG -3' NH2 CYPmut (+) C2691, 21mer, 57%GC, Tm=60C  
SEQ ID NO:32 5'- GCAGAGATGGA---GGTGAGAGTG (A) 30 -3' NH2 CYPmut (+) C2691 (A) 30-3' NH2  
SEQ ID NO:33 5'- CAGAGATGGA---GGTGAGAGTG (A) 30 -3' NH2 CYPmut (+) C2692 (A) 30-3' NH2

|-2676

SEQ ID NO:34 3'- TGACTCCGGAAGGACCGTCTTCTACCTCTTCCACTCTCACCGAGGTGCCAC -5' Wild Type (-)  
SEQ ID NO:35 3'- TGACTCCGGAAGGACCGTCTTCTACCT--CCACTCTCACCGAGGTGCCAC -5' Mut (-)

4. 'E' Allele, CYP2D6\*7, A3023C, H324P amino acid change results in zero enzyme activity

A. wt Probe - CYPwt (-) E3009 (T/C to mut at base 5) & CYPmut (+) E3009 (C/A to wt at base 15)

3023

SEQ ID NO:36 NH2 3'- CGAGTACTAGGATGTAGGC -5' CYPwt (-) E3009, 19mer, 53%GC, Pred Tm=57  
SEQ ID NO:37 NH2 3'- (A) 30CGAGTACTAGGATGTAGGC -5' CYPwt (-) E3009 (A) 30-3' NH2  
SEQ ID NO:38 5'- GCTCATGATCCTACCTCCG -3' NH2 CYPmut (+) E3009, 19mer, 58%GC, Pred Tm=59C  
SEQ ID NO:39 5'- GCTCATGATCCTACCTCCG (A) 30 -3' NH2 CYPmut (+) E3009 (A) 30-3' NH2

|-2998

SEQ ID NO:40 5'- TGGGGCCTCCTGCTCATGATCCTACATCCGGATGTGCAGC|GTGAGCCCATC -3' Wild Type (+)  
SEQ ID NO:41 5'- TGGGGCCTCCTGCTCATGATCCTACCTCCGGATGTGCAGC|GTGAGCCCATC -3' Mut (+)  
|-3038-Intron Start

B. CYPwt (-) E3018 (T/C to mut at base 14) and CYPmut (+) E3018 (C/T to wt at base 6)

SEQ ID NO:42 NH2 3'- GGATGTAGGCCTACACGTC -5' CYPwt (-) E3018, 19mer, 58%GC, Tm=60  
SEQ ID NO:43 5'- CCTACATCCGGATGTGCAG -3' CYPwt (+) E3018- Target  
SEQ ID NO:44 5'- CCTACCTCCGGATGTGCAG -3' NH2 CYPmut (+) E3018, 19mer, 63%GC, Tm=62C  
SEQ ID NO:45 3'- GGATGGAGGCCTACACGTC -5' CYPmut (-) E3018- Target

|-2998

SEQ ID NO:46 5'- TGGGGCCTCCTGCTCATGATCCTACATCCGGATGTGCAGC|GTGAGCCCATC -3' Wild Type (+)  
SEQ ID NO:47 5'- TGGGGCCTCCTGCTCATGATCCTACCTCCGGATGTGCAGC|GTGAGCCCATC -3' Mut (+)  
|-3038-Intron Start

Replacement Sheet

FIGURE 6C

5. 'G' Allele, CYP2D6*8, G1846T, Stop codon, zero enzyme activity	
SEQ ID NO:48	5'- CACTCCGGTGGGTGATGG (A) 30 -3' NH2
SEQ ID NO:49	NH2 3'- (A) 30GTGAGGCCACCCACTACC -5'
SEQ ID NO:50	5'- CACTCCTGTGGGTGATGG (A) 30 -3' NH2
SEQ ID NO:51	5'- GTGCCCGCCTTCGCCACTCC   GGTGGGTGATGGCAGAGGGCACAAGCGGG -3'
SEQ ID NO:52	5'- GTGCCCGCCTTCGCCACTCC   TGTGGGTGATGGCAGAGGGCACAAGCGGG -3'
Exon 3 end-   -1846	
6. 'T' Allele, CYP2D6*6, T1795 deletion, Frameshift resulting in zero enzyme activity	
SEQ ID NO:53	5'- GCTGGAGCAGTGGGTGAC -3' NH2
SEQ ID NO:54	5'- GCTGGAGCAGTGGGTGAC (A) 30 -3' NH2
SEQ ID NO:55	5'- CTGGAGCAGTGGGTGAC (A) 30 -3' NH2
SEQ ID NO:56	5'- GCTGGAGCAG-GGGTGAC -3' NH2
SEQ ID NO:57	5'- GCTGGAGCAG-GGGTGAC (A) 30 -3' NH2
SEQ ID NO:58	5'- CTGGAGCAG-GGGTGAC (A) 30 -3' NH2
-1773	
SEQ ID NO:59	5'-GGGCAAGAAGTCGTCGAGCAGTGGGTGACCGAGGAGCGCGCTGCCT -3'
SEQ ID NO:60	5'-GGGCAAGAAGTCGTCGAGCAG-GGGTGACCGAGGAGCGCGCTGCCT -3'
Wild Type (+) Mut (+)	
7. 2D6/2D7/2D8 Controls - The 2D6/7/8 probes were designed in the 1600 region of the 2D6 gene. The purpose of the designs was to find region somewhere between the PCR primers were it would be easy to discriminate between 2D6 and its two pseudogenes, 2D7 and 2D8. The purpose of the designs is to demonstrate that the PCR amplicon is from the 2D6 gene, not one of the pseudogenes.	
SEQ ID NO:61	5'- GACCAGGGGAGC-ATAGG (A) 30-3' NH2
SEQ ID NO:62	5'- GACCTTGTGGAGCGCCAG (A) 30-3' NH2
SEQ ID NO:63	5'- GACCAGGAAAAGC-ACAGG (A) 30-3' NH2
SEQ ID NO:64	5'- GACCAGGAAAAGC-ACAGGG (A) 30-3' NH2
-1603	
SEQ ID NO:65	5' - GGGAGACCAAGGGGAGC-ATAGGGTTGGAGTGGTGGT -3'
SEQ ID NO:66	5' - GGGAGACCTTGTGGAGCGCCAGGGTTGGAGTGGTGGC -3'
SEQ ID NO:67	5' - GGGAGACCAAGGAAAAGC-ACAGGGTTGGAGTGGGCGGC -3'
8. Pos/Neg Control probes- These probes were designed as true positive and negative control probes. They consist of the same semi-random sequence, with the positive control probe having a 5' Biotin.	
SEQ ID NO:68	5' Biotin- ATCATTCCAATCATCATCATCATC (A) 25 -3' NH2
SEQ ID NO:69	5'- ATCATTCCAATCATCATCATCATC (A) 25 -3' NH2
CYPwt (+) G1840 (A) 30-3' NH2, 18mer, 67%GC, Trn=59-61C	
CYPwt (-) G1840 (A) 30-3' NH2	
CYPmut (+) G1840 (A) 30-3' NH2, 18mer, 61%GC, Tm=57	
CYPmut (+) T1785, 17mer, 71 %GC, Tm=58-60C	
CYPmut (+) T1785 (A) 30-3' NH2	
CYPmut (+) T1786 (A) 30-3' NH2	
CYP2D6wt (+) 1607 (A) 30-3' NH2	
CYP2D7wt (+) 1607 (A) 30-3' NH2	
CYP2D8wt (+) 1607 (A) 30-3' NH2	
CYP2D8wt (+) 1607b (A) 30-3' NH2	
2D6 (+)	
2D7 (+)	
2D8 (+)	